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#13

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/750,590

DATE: 09/21/2001
TIME: 18:46:17

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF3\09212001\I750590.raw**

ENTERED

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 4 <110> APPLICANT: Ira Herman
 5        Alice Welch
 7 <120> TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL AND
 8        ABNORMAL CELL MIGRATION
10 <130> FILE REFERENCE: TUI-001CP
12 <140> CURRENT APPLICATION NUMBER: US 09/750,590
13 <141> CURRENT FILING DATE: 2000-12-28
15 <150> PRIOR APPLICATION NUMBER: 60/170,182
16 <151> PRIOR FILING DATE: 1999-12-10
18 <150> PRIOR APPLICATION NUMBER: 09/733,818
19 <151> PRIOR FILING DATE: 2000-12-08
21 <160> NUMBER OF SEQ ID NOS: 3
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4730
27 <212> TYPE: DNA
28 <213> ORGANISM: Bos taurus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (392)...(4597)
34 <400> SEQUENCE: 1
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36 gggaaggcag agaaagacat cttctaaata acaaatagga ggagttacag tacctgactt 120
37 ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
38 gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgtagtgc 240
39 agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagttagga 300
40 gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360
41 gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct    412
42                                   Met Met Ser Cys Trp Phe Ser
43                                   1               5
45 tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac   460
46 Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
47          10              15                  20
49 cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca   508
50 Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
51      25              30                  35
53 atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc   556
54 Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
55  40                  45                  50                  55
57 aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg   604
58 Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
59                  60                  65                  70
61 aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca   652
62 Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala
63                  75              80                  85
65 gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt   700
66 Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys
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67          90                    95                    100
69 cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg   748
70 Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
71     105               110                   115
73 cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct   796
74 Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
75 120               125                   130                   135
77 agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat   844
78 Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
79               140                   145                   150
81 gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca   892
82 Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro
83               155                   160                   165
85 aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga   940
86 Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg
87        170                   175                   180
89 gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc   988
90 Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys
91     185               190                   195
93 aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg   1036
94 Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu
95 200               205                   210                   215
97 ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac   1084
98 Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp
99               220                   225                   230
101 aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac  1132
102 Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn
103               235                   240                   245
105 aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat  1180
106 Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn
107        250                   255                   260
109 ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag  1228
110 Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu
111     265               270                   275
113 cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag  1276
114 His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu
115 280               285                   290                   295
117 aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc  1324
118 Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val
119               300                   305                   310
121 aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat  1372
122 Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp
123               315                   320                   325
125 ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa  1420
126 Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu
127        330                   335                   340
129 aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga  1468
130 Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg
131     345               350                   355
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133 ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg      1516
134 Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg
135 360                 365                 370   ·             375
137 aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca      1564
138 Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser
139                 380                 385                 390
141 cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg      1612
142 Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met
143                 395                 400                 405
145 tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa      1660
146 Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu
147             410                 415                 420
149 aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat      1708
150 Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp
151     425                 430                 435
153 tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag      1756
154 Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys
155 440                 445                 450                 455
157 gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag      1804
158 Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu
159                 460                 465                 470
161 gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg      1852
162 Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val
163             475                 480                 485
165 cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca      1900
166 Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr
167             490                 495                 500
169 cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg      1948
170 His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly
171     505                 510                 515
173 aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa      1996
174 Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys
175 520                 525                 530                 535
177 gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa      2044
178 Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln
179                 540                 545                 550
181 atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc      2092
182 Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly
183             555                 560                 565
185 aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt      2140
186 Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys
187         570                 575                 580
189 gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc      2188
190 Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly
191     585                 590                 595
193 cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag      2236
194 Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu
195 600                 605                 610                 615
197 aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag      2284
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198 Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys
199                 620             625                 630
201 gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat    2332
202 Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn
203             635             640             645
205 gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg    2380
206 Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu
207         650             655             660
209 gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta    2428
210 Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu
211     665             670             675
213 gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg    2476
214 Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser
215 680                 685             690                 695
217 aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat    2524
218 Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn
219                 700             705             710
221 aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat    2572
222 Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn
223             715             720             725
225 gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat gta att    2620
226 Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp Val Ile
227             730             735             740
229 gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa tat aca    2668
230 Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys Tyr Thr
231     745             750             755
233 gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc agt tta    2716
234 Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala Ser Leu
235 760                 765             770                 775
237 agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc gag aga    2764
238 Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro Glu Arg
239             780             785             790
241 cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa ctt aag    2812
242 His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu Leu Lys
243             795             800             805
245 aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa gag aaa    2860
246 Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln Glu Lys
247         810             815             820
249 ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc atg agt    2908
250 Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr Met Ser
251     825             830             835
253 cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act gcc ttg    2956
254 His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr Ala Leu
255 840             845             850             855
257 agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg aag aag    3004
258 Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val Lys Lys
259             860             865             870
261 aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat gag aac    3052
262 Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp Glu Asn
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263             875             880             885
265 gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta aaa gct    3100
266 Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val Lys Ala
267         890             895             900
269 gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc cta agg    3148
270 Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly Leu Arg
271         905             910             915
273 aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg gct aag    3196
274 Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu Ala Lys
275 920             925             930             935
277 tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag att gca    3244
278 Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu Ile Ala
279             940             945             950
281 gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag cta aaa    3292
282 Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys Leu Lys
283             955             960             965
285 tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt aaa gcc    3340
286 Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe Lys Ala
287         970             975             980
289 act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag aag tat    3388
290 Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln Lys Tyr
291         985             990             995
293 aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat gac aag    3436
294 Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn Asp Lys
295 1000            1005            1010            1015
297 tta aag aag gag atc ctc act ctt cag aag gat cta aag gat aag aat    3484
298 Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp Lys Asn
299             1020            1025            1030
301 gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc aga aaa    3532
302 Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser Arg Lys
303             1035            1040            1045
305 aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa tac aca    3580
306 Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys Tyr Thr
307         1050            1055            1060
309 gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc aag cag    3628
310 Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala Lys Gln
311     1065            1070            1075
313 act tct gag atc ctt gca gca caa act ctt ttg cag aag cag cat gtt    3676
314 Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln His Val
315 1080            1085            1090            1095
317 ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt aca atc    3724
318 Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly Thr Ile
319             1100            1105            1110
321 gag aca ctc aag gaa gaa ctg aaa act aag cag aga tgt tat gag aaa    3772
322 Glu Thr Leu Lys Glu Glu Leu Lys Thr Lys Gln Arg Cys Tyr Glu Lys
323             1115            1120            1125
325 gag cag cag aca gtg acc caa ctg cgg cag atg ctg gag aat cag aag    3820
326 Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn Gln Lys
327         1130            1135            1140
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VERIFICATION SUMMARY
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